

## SEQUENCE LISTING

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Plantechno S.r.l.

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<150> RM2002A000115

<151> 2002-01-03

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<170> PatentIn version 3.1

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acc ttt cct gcc ctt ggt acc ttc agc cgc tat gag agt aca cgc agt	192
Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser	
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Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile	
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tct gaa gaa gga atc gga tat aac atc atc cgg gta ccc atg gcc agc	432
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Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp	
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Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys	
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Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser	
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His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala	
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Gln	Ser	Val	Arg	Leu	Gly	Ser	Trp	Asp	Arg	Gly	Met	Gln	Tyr	Ser	His		
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Gly	Ser	Gln	Arg	Val	Gly	Leu	Val	Ala	Ser	Gln	Lys	Asn	Asp	Leu	Asp		
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Asn	Arg	Ser	Ser	Lys	Asp	Val	Pro	Leu	Thr	Ile	Lys	Asp	Pro	Ala	Val		
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Gly	Phe	Leu	Glu	Thr	Ile	Ser	Pro	Gly	Tyr	Ser	Ile	His	Thr	Tyr	Leu		
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Trp	His	Arg	Gln														
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Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys  
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Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile  
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Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp  
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Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro  
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Gly Cys Ala Leu Ala Leu Arg Phe Leu Ala Leu Val Ser Trp Asp Ile  
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Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala Arg Thr Pro Thr Met  
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att gat gac tgt tgg atg gct ccc caa aga gat tca gaa ggc aga ctt Ile Asp Asp Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu 60 65 70 75	341
cag gca gac cct cag cgc ttt cct cat ggg att cgc cag cta gct aat Gln Ala Asp Pro Gln Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn 80 85 90	389
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gat gcc cag acc ttt gct gac tgg gga gta gat ctg cta aaa ttt gat Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys Phe Asp 125 130 135	533
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Gln	Met	Ala	Leu	Trp	Ala	Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	
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Asp	Leu	Leu														

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Glu	Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	20	25	30	
Ile	Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	35	40	45	
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Gly	Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	115	120	125	
Ala	Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	130	135	140	
Ser	Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	145	150	155	160
Asn	Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	165	170	175	
Met	Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	180	185	190	
Asn	His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	195	200	205	
Lys	Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	210	215	220	

Val Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly  
225 230 235 240

Asn Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp  
245 250 255

Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile  
260 265 270

Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile  
275 280 285

Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp  
290 295 300

Asn Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val  
305 310 315 320

Ala Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile  
325 330 335

Ala Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe  
340 345 350

Ile Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp  
355 360 365

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
370 375 380

Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu  
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<213> Artificial Sequence

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or native signal peptide

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gcccgttggt cagcgaggga ggctctgggc ctgccgcagc tgacggggaa actgaggcac 180  
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gggcacatcc tactccatga tttcctgctg gttccccgag agctgagtgg ctctcccca 360  
gtcctggagg agactcacc agctcaccag caggagacca gcagaccagg gccccgggat 420  
gcccag gca cac ccc ggc cgt ccc aga gca gtg ccc aca cag tgc gac 468  
Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr Gln Cys Asp  
1 5 10  
gtc ccc ccc aac agc cgc ttc gat tgc gcc cct gac aag gcc atc acc 516  
Val Pro Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys Ala Ile Thr  
15 20 25 30  
cag gaa cag tgc gag gcc cgc ggc tgc tgc tac atc cct gca aag cag 564

Gln	Glu	Gln	Cys	Glu	Ala	Arg	Gly	Cys	Cys	Tyr	Ile	Pro	Ala	Lys	Gln	
				35					40					45		
ggg	ctg	cag	gga	gcc	cag	atg	ggg	cag	ccc	tgg	tgc	ttc	ttc	cca	ccc	612
Gly	Leu	Gln	Gly	Ala	Gln	Met	Gly	Gln	Pro	Trp	Cys	Phe	Phe	Pro	Pro	
			50					55					60			
agc	tac	ccc	agc	tac	aag	ctg	gag	aac	ctg	agc	tcc	tct	gaa	atg	ggc	660
Ser	Tyr	Pro	Ser	Tyr	Lys	Leu	Glu	Asn	Leu	Ser	Ser	Ser	Glu	Met	Gly	
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tac	acg	gcc	acc	ctg	acc	cgt	acc	acc	ccc	acc	ttc	ttc	ccc	aag	gac	708
Tyr	Thr	Ala	Thr	Leu	Thr	Arg	Thr	Thr	Pro	Thr	Phe	Phe	Pro	Lys	Asp	
	80					85					90					
atc	ctg	acc	ctg	cgg	ctg	gac	gtg	atg	atg	gag	act	gag	aac	cgc	ctc	756
Ile	Leu	Thr	Leu	Arg	Leu	Asp	Val	Met	Met	Glu	Thr	Glu	Asn	Arg	Leu	
95					100					105					110	
cac	ttc	acg	atc	aaa	gat	cca	gct	aac	agg	cgc	tac	gag	gtg	ccc	ttg	804
His	Phe	Thr	Ile	Lys	Asp	Pro	Ala	Asn	Arg	Arg	Tyr	Glu	Val	Pro	Leu	
				115					120					125		
gag	acc	ccg	cgt	gtc	cac	agc	cgg	gca	ccg	tcc	cca	ctc	tac	agc	gtg	852
Glu	Thr	Pro	Arg	Val	His	Ser	Arg	Ala	Pro	Ser	Pro	Leu	Tyr	Ser	Val	
			130					135					140			
gag	ttc	tcc	gag	gag	ccc	ttc	ggg	gtg	atc	gtg	cac	cgg	cag	ctg	gac	900
Glu	Phe	Ser	Glu	Glu	Pro	Phe	Gly	Val	Ile	Val	His	Arg	Gln	Leu	Asp	
		145					150					155				
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Gly	Arg	Val	Leu	Leu	Asn	Thr	Thr	Val	Ala	Pro	Leu	Phe	Phe	Ala	Asp	
	160					165					170					
cag	ttc	ctt	cag	ctg	tcc	acc	tcg	ctg	ccc	tcg	cag	tat	atc	aca	ggc	996
Gln	Phe	Leu	Gln	Leu	Ser	Thr	Ser	Leu	Pro	Ser	Gln	Tyr	Ile	Thr	Gly	
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ctc	gcc	gag	cac	ctc	agt	ccc	ctg	atg	ctc	agc	acc	agc	tgg	acc	agg	1044
Leu	Ala	Glu	His	Leu	Ser	Pro	Leu	Met	Leu	Ser	Thr	Ser	Trp	Thr	Arg	
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atc	acc	ctg	tgg	aac	cgg	gac	ctt	gcg	ccc	acg	ccc	ggt	gcg	aac	ctc	1092
Ile	Thr	Leu	Trp	Asn	Arg	Asp	Leu	Ala	Pro	Thr	Pro	Gly	Ala	Asn	Leu	
		210						215					220			
tac	ggg	tct	cac	cct	ttc	tac	ctg	gcg	ctg	gag	gac	ggc	ggg	tcg	gca	1140
Tyr	Gly	Ser	His	Pro	Phe	Tyr	Leu	Ala	Leu	Glu	Asp	Gly	Gly	Ser	Ala	
		225					230					235				
cac	ggg	gtg	ttc	ctg	cta	aac	agc	aat	gcc	atg	gat	gtg	gtc	ctg	cag	1188
His	Gly	Val	Phe	Leu	Leu	Asn	Ser	Asn	Ala	Met	Asp	Val	Val	Leu	Gln	
	240					245					250					
ccg	agc	cct	gcc	ctt	agc	tgg	agg	tcg	aca	ggt	ggg	atc	ctg	gat	gtc	1236
Pro	Ser	Pro	Ala	Leu	Ser	Trp	Arg	Ser	Thr	Gly	Gly	Ile	Leu	Asp	Val	

255	260	265	270	
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gac gtt gtg gga tac ccg ttc atg ccg cca tac tgg ggc ctg ggc ttc Asp Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe 290 295 300				1332
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gtg gag aac atg acc agg gcc cac ttc ccc ctg gac gtc caa tgg aac Val Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn 320 325 330				1428
gac ctg gac tac atg gac tcc cgg agg gac ttc acg ttc aac aag gat Asp Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp 335 340 345 350				1476
ggc ttc cgg gac ttc ccg gcc atg gtg cag gag ctg cac cag ggc ggc Gly Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His Gln Gly Gly 355 360 365				1524
cgg cgc tac atg atg atc gtg gat cct gcc atc agc agc tcg ggc cct Arg Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro 370 375 380				1572
gcc ggg agc tac agg ccc tac gac gag ggt ctg cgg agg ggg gtt ttc Ala Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe 385 390 395				1620
atc acc aac gag acc ggc cag ccg ctg att ggg aag gta tgg ccc ggg Ile Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly 400 405 410				1668
tcc act gcc ttc ccc gac ttc acc aac ccc aca gcc ctg gcc tgg tgg Ser Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp 415 420 425 430				1716
gag gac atg gtg gct gag ttc cat gac cag gtg ccc ttc gac ggc atg Glu Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Met 435 440 445				1764
tgg att gac atg aac gag cct tcc aac ttc atc aga ggc tct gag gac Trp Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp 450 455 460				1812
ggc tgc ccc aac aat gag ctg gag aac cca ccc tac gtg cct ggg gtg Gly Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val 465 470 475				1860
gtt ggg ggg acc ctc cag gcg gcc acc atc tgt gcc tcc agc cac cag Val Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln 480 485 490				1908

ttt ctc tcc aca cac tac aac ctg cac aac ctc tac ggc ctg acc gaa Phe Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu 495 500 505 510	1956
gcc atc gcc tcc cac agg gcg ctg gtg aag gct cgg ggg aca cgc cca Ala Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro 515 520 525	2004
ttt gtg atc tcc cgc tcg acc ttt gct ggc cac ggc cga tac gcc ggc Phe Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly 530 535 540	2052
cac tgg acg ggg gac gtg tgg agc tcc tgg gag cag ctc gcc tcc tcc His Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser 545 550 555	2100
gtg cca gaa atc ctg cag ttt aac ctg ctg ggg gtg cct ctg gtc ggg Val Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro Leu Val Gly 560 565 570	2148
gcc gac gtc tgc ggc ttc ctg ggc aac acc tca gag gag ctg tgt gtg Ala Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val 575 580 585 590	2196
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cag cag gcc atg agg aag gcc ctc acc ctg cgc tac gca ctc ctc ccc Gln Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala Leu Leu Pro 625 630 635	2340
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gcc cgg ccc ctc ttc ctg gag ttc ccc aag gac tct agc acc tgg act Ala Arg Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser Thr Trp Thr 655 660 665 670	2436
gtg gac cac cag ctc ctg tgg ggg gag gcc ctg ctc atc acc cca gtg Val Asp His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile Thr Pro Val 675 680 685	2484
ctc cag gcc ggg aag gcc gaa gtg act ggc tac ttc ccc ttg ggc aca Leu Gln Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro Leu Gly Thr 690 695 700	2532
tgg tac gac ctg cag acg gtg cca ata gag gcc ctt ggc agc ctc cca Trp Tyr Asp Leu Gln Thr Val Pro Ile Glu Ala Leu Gly Ser Leu Pro 705 710 715	2580



ccc cca cct gca gct ccc cgt gag cca gcc atc cac agc gag ggg cag Pro Pro Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln 720 725 730	2628
tgg gtg acg ctg ccg gcc ccc ctg gac acc atc aac gtc cac ctc cgg Trp Val Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg 735 740 745 750	2676
gct ggg tac atc atc ccc ctg cag ggc cct ggc ctc aca acc aca gag Ala Gly Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu 755 760 765	2724
tcc cgc cag cag ccc atg gcc ctg gct gtg gcc ctg acc aag ggt gga Ser Arg Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly 770 775 780	2772
gag gcc cga ggg gag ctg ttc tgg gac gat gga gag agc ctg gaa gtg Glu Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val 785 790 795	2820
ctg gag cga ggg gcc tac aca cag gtc atc ttc ctg gcc agg aat aac Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn Asn 800 805 810	2868
acg atc gtg aat gag ctg gta cgt gtg acc agt gag gga gct ggc ctg Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala Gly Leu 815 820 825 830	2916
cag ctg cag aag gtg act gtc ctg ggc gtg gcc acg gcg ccc cag cag Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala Pro Gln Gln 835 840 845	2964
gtc ctc tcc aac ggt gtc cct gtc tcc aac ttc acc tac agc ccc gac Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr Ser Pro Asp 850 855 860	3012
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Thr Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu Val Pro Leu Glu Thr  
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Pro Arg Val His Ser Arg Ala Pro Ser Pro Leu Tyr Ser Val Glu Phe  
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Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe Phe Ala Asp Gln Phe  
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Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr Ile Thr Gly Leu Ala  
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Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg Ile Thr  
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Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu Tyr Gly  
210 215 220

Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala His Gly  
225 230 235 240

Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln Pro Ser  
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Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val Tyr Ile  
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Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu Asp Val  
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Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe His Leu  
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Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val Val Glu  
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325 330 335

Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp Gly Phe  
340 345 350

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Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro Ala Gly  
370 375 380

Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe Ile Thr  
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Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly Ser Thr

405

410

415

Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp Glu Asp  
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Met Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Met Trp Ile  
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Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp Gly Cys  
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Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val Val Gly  
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Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln Phe Leu  
 485 490 495

Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu Ala Ile  
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Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro Phe Val  
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Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly His Trp  
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Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro Leu Val Gly Ala Asp  
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Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val Arg Trp  
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Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg Asn His Asn Ser Leu  
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Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser Glu Pro Ala Gln Gln  
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Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala Leu Leu Pro His Leu  
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Tyr Thr Leu Phe His Gln Ala His Val Ala Gly Glu Thr Val Ala Arg  
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Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser Thr Trp Thr Val Asp  
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His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile Thr Pro Val Leu Gln  
675 680 685

Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp Tyr  
690 695 700

Asp Leu Gln Thr Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro Pro  
705 710 715 720

Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp Val  
725 730 735

Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala Gly  
740 745 750

Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser Arg  
755 760 765

Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu Ala  
770 775 780

Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val Leu Glu  
785 790 795 800

Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn Asn Thr Ile  
805 810 815

Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala Gly Leu Gln Leu  
820 825 830

Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala Pro Gln Gln Val Leu  
835 840 845

Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr Ser Pro Asp Thr Lys  
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or native signal peptide

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